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Epigenetics in lung cancer diagnosis and therapy

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Abstract

© 2015, Springer Science+Business Media New York. Lung cancer is the leading cause of cancer-related deaths worldwide. The initiation and progression of lung cancer is the result of the interaction between permanent genetic and dynamic epigenetic alterations. DNA methylation is the best studied epigenetic mark in human cancers. Altered DNA methylation in cancer was identified in 1983. Within 30 years of this discovery, DNA methylation inhibitors are used clinically to treat a variety of cancers, highlighting the importance of the epigenetic basis of cancer. In addition, histone modifications, nucleosome remodeling, and micro RNA (miRNA)-mediated gene regulation are also fundamental to tumor genesis. Distinct chromatin alterations occur in all stages of lung cancer, including initiation, growth, and metastasis. Therefore, stage-specific epigenetic changes can be used as powerful and reliable tools for early diagnosis of lung cancer and to monitor patient prognosis. Moreover, since epigenetic changes are dynamic and reversible, chromatin modifiers are promising targets for the development of more effective therapeutic strategies against cancer. This review summarizes the chromatin alterations in lung cancer, focusing on the diagnostic and therapeutic approaches targeting epigenetic modifications that could help to reduce the high case-fatality rate of this dreadful disease.

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Keywords

Chromatin, DNA methylation, Early diagnosis, Epigenetics, Histone modifications, Lung cancer, Metastasis, miRNA, Treatment